



SEQUENCE LISTING

<110> E. I. du Pont de Nemours and Company

<120> Flavonoid Biosynthetic Enzymes

<130> BB1324

<140> 09/868,546

<141> 2001-09-20

<150> 60/113,190

<151> 1998-12-21

<160> 6

<170> Microsoft Office 97

<210> 1

<211> 1859

<212> DNA

<213> Glycine max

<400> 1

gaaaacactg	acagacagca	tagtctcttg	tgcaagaatc	aattgagcaa	gcatgggaat	60
gttggtggtg	gtggtctcat	acgctgtcct	tttctggtt	ctattcctcg	gcgtgaagtt	120
gtttttccaa	agcagaaaat	tgagaaacat	accaccaggt	cctcctcctc	ttcccataat	180
aggaaacctt	aacctcctcg	aacagccaat	ccaccgtttc	ttccaacgca	tgctgaaaca	240
gtacggcaac	gtggtttccc	tctggttcgg	ttcacgtctg	gccgttgtca	tctcctctcc	300
aacagcatac	caagaatgct	tcaccaaaac	cgacgttgcc	ttggccaacc	ggctaccttc	360
tctctcgggg	aaatacatct	tctacaacaa	caccaccgta	ggctcctgct	cccacggcga	420
gcactggcgc	aacctccgcc	gcacacccgc	cctggacgtc	ctctccacgc	agcgcgtcca	480
ctcctttctc	ggaatccgga	gcgacgagac	gaagcgtctg	atgcagaggt	tggtgctggc	540
caagaactcg	aacgaggaag	agtttgcgcg	agtggagatt	agttcgatgt	tcaacgactt	600
aacttacaac	aacataatga	ggatgataat	ggggaagagg	ttttacggag	aggagagtga	660
gatgaagaac	gttgaggaag	cgagggagtt	cagagagact	gtgacagaaa	tggtggaact	720
catgggcttg	gctaacaagg	gagatcactt	gcctttcctc	aggtggttcg	attttcagaa	780
tgtggagaag	cgcttaaaga	gtatcagtaa	gaggtacgat	tccatcttga	ataagatcct	840
tcatgagaac	cgtgccagca	atgaccgcca	gaattccatg	atcgatcatc	tcctcaaact	900
gcaagagacc	cagcctcagt	actacactga	ccaaatcatc	aaaggccttg	ctctggccat	960
gcttttttgt	ggaactgact	catcaactgg	gacttttagag	tggtcattat	ctaattttatt	1020
gaatcaccca	gaggtgttga	agaaggcaag	agatgaattg	gacactcaag	tgggacaaga	1080
ccgcttggtt	aatgagtcag	accttccaaa	acttccatat	cttaggaaga	tcaccttga	1140
gacacttagg	ttgtaccccc	cggccccaat	tctaatacct	catgtgtctt	cagaagatat	1200
tacaattgaa	ggattcaata	tcccacgaga	cacaattgtg	atcattaatg	gttggggcat	1260
gcagagagat	cctcagttgt	ggaatgatgc	cacatgcttt	aaacctgaga	ggtttgatgt	1320
ggaaggagag	gagaaaaagt	tggtagcatt	tggcatggga	agaagggtt	gccaggaga	1380
acccatggct	atgcaaagtg	tcagctttac	tttgggattg	ttgattcaat	gttttgactg	1440
gaaacgagta	agtgaggaaa	agcttgatat	gacagagaac	aattggatca	ccttgtcaag	1500
gttaattcca	ttggaggcca	tgtgcaaggc	tcgcccactt	gccactaaaa	ttggaattta	1560
attattaata	gtatttttat	ttggtaaaat	tgggtgattc	agaatctaata	acttataatt	1620
ttagtggtga	agagtgggtga	tcatatatac	atttcaaaat	taataatctt	tgccaaaaaa	1680
tcattccatg	acaactatat	gtcaattgac	atctagagag	aaatatagat	ataagaatat	1740
ttatatttta	ttactcttct	ttatcttatg	tgtcaaggcc	cattgtagaa	ttgggtgagc	1800
attaacatat	atcaatatgt	tataccgccc	agttttctca	aataaatttc	tttactttc	1859

<210> 2

<211> 499

<212> PRT

<213> Glycine max

<400> 2

Leu Leu Val Val Val Ser Tyr Ala Val Leu Phe Leu Val Leu Phe Leu
1 5 10 15
Gly Val Lys Phe Val Phe Gln Ser Arg Lys Leu Arg Asn Ile Pro Pro
20 25 30
Gly Pro Pro Pro Leu Pro Ile Ile Gly Asn Leu Asn Leu Leu Glu Gln
35 40 45
Pro Ile His Arg Phe Phe Gln Arg Met Ser Lys Gln Tyr Gly Asn Val
50 55 60
Val Ser Leu Trp Phe Gly Ser Arg Leu Ala Val Val Ile Ser Ser Pro
65 70 75 80
Thr Ala Tyr Gln Glu Cys Phe Thr Lys His Asp Val Ala Leu Ala Asn
85 90 95
Arg Leu Pro Ser Leu Ser Gly Lys Tyr Ile Phe Tyr Asn Asn Thr Thr
100 105 110
Val Gly Ser Cys Ser His Gly Glu His Trp Arg Asn Leu Arg Arg Ile
115 120 125
Thr Ala Leu Asp Val Leu Ser Thr Gln Arg Val His Ser Phe Ser Gly
130 135 140
Ile Arg Ser Asp Glu Thr Lys Arg Leu Met Gln Arg Leu Val Leu Ala
145 150 155 160
Lys Asn Ser Asn Glu Glu Glu Phe Ala Arg Val Glu Ile Ser Ser Met
165 170 175
Phe Asn Asp Leu Thr Tyr Asn Asn Ile Met Arg Met Ile Ser Gly Lys
180 185 190
Arg Phe Tyr Gly Glu Glu Ser Glu Met Lys Asn Val Glu Glu Ala Arg
195 200 205
Glu Phe Arg Glu Thr Val Thr Glu Met Leu Glu Leu Met Gly Leu Ala
210 215 220
Asn Lys Gly Asp His Leu Pro Phe Leu Arg Trp Phe Asp Phe Gln Asn
225 230 235 240
Val Glu Lys Arg Leu Lys Ser Ile Ser Lys Arg Tyr Asp Ser Ile Leu
245 250 255
Asn Lys Ile Leu His Glu Asn Arg Ala Ser Asn Asp Arg Gln Asn Ser
260 265 270
Met Ile Asp His Leu Leu Lys Leu Gln Glu Thr Gln Pro Gln Tyr Tyr
275 280 285
Thr Asp Gln Ile Ile Lys Gly Leu Ala Leu Ala Met Leu Phe Gly Gly
290 295 300

Thr Asp Ser Ser Thr Gly Thr Leu Glu Trp Ser Leu Ser Asn Leu Leu
 305 310 315 320
 Asn His Pro Glu Val Leu Lys Lys Ala Arg Asp Glu Leu Asp Thr Gln
 325 330 335
 Val Gly Gln Asp Arg Leu Leu Asn Glu Ser Asp Leu Pro Lys Leu Pro
 340 345 350
 Tyr Leu Arg Lys Ile Ile Leu Glu Thr Leu Arg Leu Tyr Pro Pro Ala
 355 360 365
 Pro Ile Leu Ile Pro His Val Ser Ser Glu Asp Ile Thr Ile Glu Gly
 370 375 380
 Phe Asn Ile Pro Arg Asp Thr Ile Val Ile Ile Asn Gly Trp Gly Met
 385 390 395 400
 Gln Arg Asp Pro Gln Leu Trp Asn Asp Ala Thr Cys Phe Lys Pro Glu
 405 410 415
 Arg Phe Asp Val Glu Gly Glu Glu Lys Lys Leu Val Ala Phe Gly Met
 420 425 430
 Gly Arg Arg Ala Cys Pro Gly Glu Pro Met Ala Met Gln Ser Val Ser
 435 440 445
 Phe Thr Leu Gly Leu Leu Ile Gln Cys Phe Asp Trp Lys Arg Val Ser
 450 455 460
 Glu Glu Lys Leu Asp Met Thr Glu Asn Asn Trp Ile Thr Leu Ser Arg
 465 470 475 480
 Leu Ile Pro Leu Glu Ala Met Cys Lys Ala Arg Pro Leu Ala Thr Lys
 485 490 495

Ile Gly Ile

<210> 3
 <211> 1698
 <212> DNA
 <213> Glycine max

<400> 3
 cagtaataac aatgtctcct ttcttatctt actctcttct ttccctcgtg ttctttcttca 60
 ctctcaagta cctttttccaa agaagcagaa aagtacgaaa cctgccacct ggtccgactc 120
 ctcttcctat aatcggcaac cttaacctcg ttgaacaacc tatacaccgt ttcttccacc 180
 gcatgtccca aaaatatgga aacatcatat ccctttggtt tgggtcacgt cttgttggtg 240
 ttgtttcatc acccacagcg taccaagaat gtttcaccaa acatgatgtt accttggcca 300
 acagggtacg ctccctctcg ggaaaataca tattctacga caacaccacc gtagggctct 360
 gctcccacgg cgagcactgg cgcaacctcc gccgcataac ctctctcgac gttctatcga 420
 cgcagcgctt ccactccttc tccggaatcc ggagcgacga gacgaagagg ttgatacaca 480
 ggctggccag ggactccggg aaagattttg cgcgctgga gatgacctcc aagtttgctg 540
 acttgacgta caacaacatc atgaggatga ttctggggaa gcggttttac ggagaagaga 600
 gtgaacttaa caacgttgag gaagcgaagg agttcagaga cactgtgaat gagatgctgc 660
 aactcatggg gttggctaac aaggagatc acttaccttt cctaaggtgg ttcgattttc 720
 agaacgtgga gaagagggtg aagaatatca gtaagaggta tgataccatc ttgaataaga 780
 tccttgatga gaaccgtaac aacaaggacc gcgagaattc catgattggt catctcctca 840
 aactgcaaga gacacagcct gactattata ccgaccaaatt catcaaaggc cttgcttttg 900

ctatgctctt tgggtggaaca gactcgtcaa ctggaacttt agagtgggca ttatctaatt 960
 tagtgaatga cccagaggtg ctgcagaagg caagagatga gttggacgct caagtaggac 1020
 cagatcggct gttaaatgag tcagaccttc caaaacttcc ttatctcagg aagatagttc 1080
 ttgaaacact taggttgtag cctccggctc caattctaatt accacacgtg gcttcagaag 1140
 acatcaatat cgaaggattc aatgttccac gagacacaat tgtgattatt aatgggtggg 1200
 ccatgcaaag agatcctaag atatggaaag atgcgacaag ctttaaacct gagagggttg 1260
 atgaagaagg agaggagaag aaattggtag catttggtat gggaagaagg gcttgcccag 1320
 gagaacccat ggctatgcaa agtggttagct atactttggg attaatgatt caatgttttg 1380
 actggaaacg agtaagtgag aagaagcttg atatgacaga gaataattgg atcaccttgt 1440
 caagggttaat tccattggag gctatgtgta aagcccggcc actcgccagc aaagttgaaa 1500
 gttattaaca atattttatt tggatatattt ggggtaggat ctaataactca taatttcggg 1560
 gtgtaagtct atgcatgtta aaattaataa tatttgcgt atgtccacaa ggccaaatgt 1620
 agtactgggt gtggatttgc atatacaata tcaatattgt ataaatccca gtttccttga 1680
 ataaatttct ttactttc 1698

<210> 4
 <211> 494
 <212> PRT
 <213> Glycine max

<400> 4
 Leu Ser Tyr Ser Leu Leu Ser Leu Val Phe Phe Phe Thr Leu Lys Tyr
 1 5 10 15
 Leu Phe Gln Arg Ser Arg Lys Val Arg Asn Leu Pro Pro Gly Pro Thr
 20 25 30
 Pro Leu Pro Ile Ile Gly Asn Leu Asn Leu Val Glu Gln Pro Ile His
 35 40 45
 Arg Phe Phe His Arg Met Ser Gln Lys Tyr Gly Asn Ile Ile Ser Leu
 50 55 60
 Trp Phe Gly Ser Arg Leu Val Val Val Val Ser Ser Pro Thr Ala Tyr
 65 70 75 80
 Gln Glu Cys Phe Thr Lys His Asp Val Thr Leu Ala Asn Arg Val Arg
 85 90 95
 Ser Leu Ser Gly Lys Tyr Ile Phe Tyr Asp Asn Thr Thr Val Gly Ser
 100 105 110
 Cys Ser His Gly Glu His Trp Arg Asn Leu Arg Arg Ile Thr Ser Leu
 115 120 125
 Asp Val Leu Ser Thr Gln Arg Val His Ser Phe Ser Gly Ile Arg Ser
 130 135 140
 Asp Glu Thr Lys Arg Leu Ile His Arg Leu Ala Arg Asp Ser Gly Lys
 145 150 155 160
 Asp Phe Ala Arg Val Glu Met Thr Ser Lys Phe Ala Asp Leu Thr Tyr
 165 170 175
 Asn Asn Ile Met Arg Met Ile Ser Gly Lys Arg Phe Tyr Gly Glu Glu
 180 185 190
 Ser Glu Leu Asn Asn Val Glu Glu Ala Lys Glu Phe Arg Asp Thr Val
 195 200 205

Asn Glu Met Leu Gln Leu Met Gly Leu Ala Asn Lys Gly Asp His Leu
 210 215 220
 Pro Phe Leu Arg Trp Phe Asp Phe Gln Asn Val Glu Lys Arg Leu Lys
 225 230 235 240
 Asn Ile Ser Lys Arg Tyr Asp Thr Ile Leu Asn Lys Ile Leu Asp Glu
 245 250 255
 Asn Arg Asn Asn Lys Asp Arg Glu Asn Ser Met Ile Gly His Leu Leu
 260 265 270
 Lys Leu Gln Glu Thr Gln Pro Asp Tyr Tyr Thr Asp Gln Ile Ile Lys
 275 280 285
 Gly Leu Ala Leu Ala Met Leu Phe Gly Gly Thr Asp Ser Ser Thr Gly
 290 295 300
 Thr Leu Glu Trp Ala Leu Ser Asn Leu Val Asn Asp Pro Glu Val Leu
 305 310 315 320
 Gln Lys Ala Arg Asp Glu Leu Asp Ala Gln Val Gly Pro Asp Arg Leu
 325 330 335
 Leu Asn Glu Ser Asp Leu Pro Lys Leu Pro Tyr Leu Arg Lys Ile Val
 340 345 350
 Leu Glu Thr Leu Arg Leu Tyr Pro Pro Ala Pro Ile Leu Ile Pro His
 355 360 365
 Val Ala Ser Glu Asp Ile Asn Ile Glu Gly Phe Asn Val Pro Arg Asp
 370 375 380
 Thr Ile Val Ile Ile Asn Gly Trp Ala Met Gln Arg Asp Pro Lys Ile
 385 390 395 400
 Trp Lys Asp Ala Thr Ser Phe Lys Pro Glu Arg Phe Asp Glu Glu Gly
 405 410 415
 Glu Glu Lys Lys Leu Val Ala Phe Gly Met Gly Arg Arg Ala Cys Pro
 420 425 430
 Gly Glu Pro Met Ala Met Gln Ser Val Ser Tyr Thr Leu Gly Leu Met
 435 440 445
 Ile Gln Cys Phe Asp Trp Lys Arg Val Ser Glu Lys Lys Leu Asp Met
 450 455 460
 Thr Glu Asn Asn Trp Ile Thr Leu Ser Arg Leu Ile Pro Leu Glu Ala
 465 470 475 480
 Met Cys Lys Ala Arg Pro Leu Ala Ser Lys Val Glu Ser Tyr
 485 490

<210> 5
 <211> 843
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (476)
 <223> n = a, c, g or t

<220>
 <221> unsure
 <222> (657)
 <223> n = a, c, g or t

<220>
 <221> unsure
 <222> (703)
 <223> n = a, c, g or t

<220>
 <221> unsure
 <222> (712)
 <223> n = a, c, g or t

<220>
 <221> unsure
 <222> (789)
 <223> n = a, c, g or t

<220>
 <221> unsure
 <222> (843)
 <223> n = a, c, g or t

<400> 5
 ttcactctca agcttcaagc atgactcctt tttacttctt cctatttgcc ttcactcctt 60
 tcctctccat aaacttcttg atccaaacaa gaagggtcaa aaaccttctt ccggggaccat 120
 tttctttccc tataatcgga aacctccacc aactcaagca acccctccac cgcacgttcc 180
 atgccttata acaaaaatat ggccctattt tctccctctg gttcggctcc cgttttgctg 240
 tcgtcgtttc gtcgccgctc gcggtgcaag aatgcttcac caagaacgac atcgtcttgg 300
 ccaaccgccc tcacttcttc accggcaagt atatagggtta caacaacacc accgtcgccg 360
 tttcccccta cggcgaccac tggcgcaacc tccgccgcat catggcgctc gaggttctct 420
 ccaccaccg gataaactcc ttcttggaaa atcggagggg acgaagatca tgaggntcgt 480
 gcaaaagctt gctcgggact cgcgcaatgg gtccaccaa gtagaactta aatccagggt 540
 ttcggagatg acattttaaca ctataatgag gatggtgtca gggaagaggt actatggtga 600
 agactgtgat gtgagtgatg tacaggaagc aagcaattta gagagatcat taaagantgg 660
 tgacgttagg aggggctaata aacctgggga ctcttggttt gcntggtggt tntttgatgg 720
 ttggaaagag ctaaagagga tagtagagaa cgatcgttta caggaccatt gtagcatcta 780
 tggaacacnt gcatacatga taatatctct gccacacaac acaccgatat aacgttaatc 840
 atn 843

<210> 6
 <211> 141
 <212> PRT
 <213> Glycine max

<400> 6
 Phe Leu Leu Phe Ala Phe Ile Leu Phe Leu Ser Ile Asn Phe Leu Ile
 1 5 10 15
 Gln Thr Arg Arg Phe Lys Asn Leu Pro Pro Gly Pro Phe Ser Phe Pro
 20 25 30
 Ile Ile Gly Asn Leu His Gln Leu Lys Gln Pro Leu His Arg Thr Phe

	35		40		45												
His	Ala	Leu	Ser	Gln	Lys	Tyr	Gly	Pro	Ile	Phe	Ser	Leu	Trp	Phe	Gly		
	50					55					60						
Ser	Arg	Phe	Val	Val	Val	Val	Ser	Ser	Pro	Leu	Ala	Val	Gln	Glu	Cys		
65					70					75					80		
Phe	Thr	Lys	Asn	Asp	Ile	Val	Leu	Ala	Asn	Arg	Pro	His	Phe	Leu	Thr		
				85					90					95			
Gly	Lys	Tyr	Ile	Gly	Tyr	Asn	Asn	Thr	Thr	Val	Ala	Val	Ser	Pro	Tyr		
			100					105					110				
Gly	Asp	His	Trp	Arg	Asn	Leu	Arg	Arg	Ile	Met	Ala	Leu	Glu	Val	Leu		
	115						120					125					
Ser	Thr	His	Arg	Ile	Asn	Ser	Phe	Leu	Glu	Asn	Arg	Arg					
130						135					140						